What is claimed is:

1.   A method for comparing a first microarray spot with a second microarray spot

comprising:

        providing a first plurality of intensity values (S_i^A) for said first microarray

spot and a second plurality of intensity values (S_k^B) for said second microarray

spot;

        calculating a p value using Wilcoxon's rank sum test, wherein said p value

is for a null hypothesis that $\theta=0$ and an alternative hypothesis that said $\theta>0$,

wherein said θ is a test statistic for intensity difference between said first plurality

and said second plurality; and

        indicating said first microarray spot is different from said second

microarray spot if said p value is greater than a significance level.

2.   The method of Claim 1 wherein said testing statistic is *median (S_i^A)-median(S_k^B).*

3.   The method of Claim 2 wherein said significance level is 0.05.

4.   The method of Claim 1 wherein said first microarray spot and second microarray

spot are nucleic acid spots.

5.   The method of Claim 4 wherein said nucleic acid spots are among at least 100

nucleic acid spots on a substrate.

6. The method of Claim 5 wherein said nucleic acid spots are among at least 1000 spots on said substrate.

7. The method of Claim 6 wherein said nucleic acid spots are cDNA spots.

8. The method of Claim 7 wherein said nucleic acid spots are oligonucleotide spots.

9. The method of Claim 1 further comprising step of combining first plurality and second plurality of intensity values if said p-value is greater than a significance level.

10. A computer software product for comparing a first microarray spot with a second microarray spot comprising:

computer program code for inputing a first plurality of intensity values (S_i^A) for said first microarray spot and a second plurality of intensity values (S_k^B) for said second microarray spot;

computer program code for calculating a p value using Wilcoxon's rank sum test, wherein said p value is for a null hypothesis that $\theta=0$ and an alternative hypothesis that said $\theta>0$, wherein said θ is a test statistic for intensity difference between said first plurality and said second plurality; and

computer program code for indicating said first microarray spot is different from said second microarray spot if said *p* value is greater than a significance level; and

a computer readable media for storing said computer program codes.

11. The computer program product of Claim 10 wherein said testing statistic is median (S_i^A)-median(S_k^B).

12. The computer program of Claim 11 wherein said significance level is 0.05.

13. The computer software product of Claim 11 further comprising computer program code for accepting user's input or selection of said significance level.

14. The computer software product of Claim 11 wherein said first microarray spot and second microarray spot are nucleic acid spots.

15. The computer software product of Claim 14 wherein said nucleic acid spots are among at least 100 nucleic acid spots on a substrate.

16. The computer software product of Claim 15 wherein said nucleic acid spots are among at least 1000 spots on said substrate.

17.   The computer software product of Claim 16 wherein said nucleic acid spots are cDNA spots.

18.   The computer software product of Claim 16 wherein said nucleic acid spots are oligonucleotide spots.

19.   The computer software product of Claim 10 further computer program code for combining first plurality and second plurality of intensity values if said p-value is greater than a significance level.

20.   The computer software product of Claim 19 wherein said significance level is 0.5.

21.   A system for comparing nucleic acid probes, comprising:

a processor; and

a memory being coupled to the processor, the memory storing a plurality machine instructions that cause the processor to perform a plurality of logical steps when implemented by the processor, said logical steps including:

inputing a first plurality of intensity values (S_i^A) for said first microarray spot and a second plurality of intensity values (S_k^B) for said second microarray spot;

calculating a p value using Wilcoxon's rank sum test, wherein said p value is for a null hypothesis that $\theta=0$ and an alternative hypothesis that said $\theta>0$,

wherein said θ is a test statistic for intensity difference between said first plurality

and said second plurality; and

indicating said first microarray spot is different from said second

microarray spot if said p value is greater than a significance level.

22.   The system of Claim 21 wherein said testing statistic is *median (S_i^A)-*

median(S_k^B).

23.   The system of Claim 22 wherein said significance level is 0.05.

24.   The system of Claim 22 wherein said steps further comprise accepting user's

input or selection of said significance level.

25.   The system of Claim 21 wherein said first microarray spot and second microarray

spot are nucleic acid spots.

26.   The system of Claim 25 wherein said nucleic acid spots are among at least 100

nucleic acid spots on a substrate.

27.   The system of Claim 26 wherein said nucleic acid spots are among at least 1000

spots on said substrate.

28. The system of Claim 27 wherein said nucleic acid spots are cDNA spots.

29. The system of Claim 27 wherein said nucleic acid spots are oligonucleotide spots.

30. The system of Claim 21 wherein said steps further comprise combining first plurality and second plurality of intensity values if said p-value is greater than a significance level.

31. The system of Claim 30 wherein said significance level is 0.5.

32. A method for determining whether a transcript is present in a biological sample comprising:

   providing a plurality of perfect match pixel intensity values (PM_{ij}) and mismatch pixel intensity values (MM_{ik}) for the transcript, wherein said PM_{ij} is the pixel intensity value for perfect match probe i and pixel j and MM_{ik} is the pixel intensity value for mismatch probe i and pixel k;

   calculating a p-value using one-sided Wilcoxon's rank sum test, wherein the p-value is for a null hypothesis that ($median(PM_{ij})$-$median(MM_{ik})$)=a threshold value and an alternative hypothesis that said ($median(PM_{ij})$-$median(MM_{ik})$)> said threshold value; and

   indicating whether said transcript is present based upon said p-value.

33.   The method of Claim 32 wherein said threshold value is zero.

34.   The method of Claim 32 wherein said threshold value is calculated

using: $\tau = c \sqrt{median(PM_i)}$ wherein said c is a constant.

35.   The method of Claim 32 wherein threshold value is calculated

using: $\tau = c_1 \sqrt{mean(PM_i)}$ wherein said c is a constant.

36.   The method of Claim 32 wherein said step of indicating comprises indicating said

transcript is present if said p is smaller than a first significance level (α_1).

37.   The method of Claim 32 wherein said step of indicating further comprises

indicating said transcript is absent if said p is greater than or equal to a second

significance level (α_2).

38.   The method of Claim 37 wherein said step of indicating further comprises

indicating said transcript is marginally detected if $\alpha_1 \le p < \alpha_2$.

39.   A computer software product for determining whether a transcript is present in a

biological sample comprising:

computer program code for inputting a plurality of perfect match pixel intensity values (PM_{ij}) and mismatch pixel intensity values (MM_{ik}) for said transcript, wherein said PM_{ij} is the pixel intensity value for perfect match probe i and pixel j and MM_{ik} is the pixel intensity value for mismatch probe i and pixel k;

computer software code for calculating a p-value using one-sided Wilcoxon's rank sum test, wherein the p-value is for a null hypothesis that $(median(PM_{ij})-median(MM_{ik}))$=a threshold value and an alternative hypothesis that said $(median(PM_{ij})-median(MM_{ik}))$> said threshold value;

computer software code for indicating whether said transcript is present based upon said p-value; and

a computer readable media for storing said code.

40. The computer software product of Claim 32 wherein said threshold value is zero.

41. The computer software product of Claim 32 wherein said threshold value is calculated using: $\tau = c \sqrt{median(PM_i)}$ wherein said c is a constant.

42. The computer software product of Claim 32 wherein threshold value is calculated using: $\tau = c_1 \sqrt{mean(PM_i)}$ wherein said c is a constant.

43. The computer software product of Claim 32 wherein said computer program code for indicating comprises computer software code for indicating that said transcript is present if said p is smaller than a first significance level (α_1).

44. The computer software product of Claim 32 wherein said computer program code for indicating further comprises computer software code for indicating said transcript is absent if said p is greater than or equal to a second significance level (α_2).

45. The computer software product of Claim 37 wherein said computer program code for indicating further comprises computer software code for indicating that said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

46. A system for comparing nucleic acid probes, comprising:

a processor; and

a memory being coupled to the processor, the memory storing a plurality machine instructions that cause the processor to perform a plurality of logical steps when implemented by the processor, said logical steps including:

providing a plurality of perfect match pixel intensity values (PM_{ij}) and mismatch pixel intensity values (MM_{ik}) for the transcript, wherein said PM_{ij} is the pixel intensity value for perfect match probe i and pixel j and MM_{ik} is the pixel intensity value for mismatch probe i and pixel k;

calculating a *p*-value using one-sided Wilcoxon's rank sum test, wherein

the *p*-value is for a null hypothesis that $(median(PM_{ij})\text{-}median(MM_{ik}))$=a

threshold value and an alternative hypothesis that said $(median(PM_{ij})\text{-}$

$median(MM_{ik}))$> said threshold value; and

5   indicating whether said transcript is present based upon said *p*-value.

47.   The system of Claim 46 wherein said threshold value is zero.

48.   The system of Claim 47 wherein said threshold value is calculated

10   using: $\tau = c\sqrt{median(PM_i)}$ wherein said *c* is a constant.

49.   The system of Claim 47 wherein threshold value is calculated

using: $\tau = c_1\sqrt{mean(PM_i)}$ wherein said *c* is a constant.

15   50.   The system of Claim 46 wherein said step of indicating comprises indicating said

transcript is present if said *p* is smaller than a first significance level (α_1).

51.   The system of Claim 50 wherein said step of indicating further comprises

indicating said transcript is absent if said *p* is greater than or equal to a second

20   significance level (α_2).

52. The system of Claim 51 wherein said first significance level (α_1) is smaller than said (α_2) and said step of indicating further comprises indicating said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

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